(1) GENERAL INFORMATION:

(i) APPLICANTS: Boon-Falleur, Thierry; Van der Bruggen, Thierry; Van den Eynde, Benoît; Van Pel, Aline; De Plaen, Etienne; Lurquin, Christophe; Chomez, Patrick; Traversari, Catia

(ii) TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor Rejection Antigens and Uses Thereof

(iii) NUMBER OF SEQUENCES: 26

(iv) CORRESPONDENCE ADDRESS:
    (A) ADDRESSEE: Fulbright & Jaworski LLP
    (B) STREET: 666 Fifth Avenue
    (C) CITY: New York City
    (D) STATE: New York
    (E) COUNTRY; USA
    (F) ZIP: 10103

(v) COMPUTER READABLE FORM:
    (A) MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
    (B) COMPUTER: IBM
    (C) OPERATING SYSTEM: PC-DOS
    (D) SOFTWARE: Wordperfect

(vi) CURRENT APPLICATION DATA:
    (A) APPLICATION NUMBER: 08/819,669
    (B) FILING DATE: 17-March-1997
    (C) CLASSIFICATION: 435

(vii) PRIOR APPLIATION DATA:
    (A) APPLICATION NUMBER: 08/142,368
    (B) FILING DATE: 02-MAY-1994

(vii) PRIOR APPLICATION DATA:
    (A) APPLICATION NUMBER: PCT/US92/04354
    (B) FILING DATE: 22-MAY-1992

(vii) PRIOR APPLICATION DATA:
    (A) APPLICATION NUMBER: 07/807,043
    (B) FILING DATE: 12-DECEMBER-1991

(vii) PRIOR APPLICATION DATA:
    (A) APPLICATION NUMBER: 07/764,364
    (B) FILING DATE: 23-SEPTEMBER-1991

(vii) PRIOR APPLICATION DATA:
    (A) APPLICATION NUMBER: 07/728,838
    (b) FILING DATE: 9-JULY-1991

(vii) PRIOR APPLICATION DATA:

576670.1

(A) APPLICATION NUMBER: 07/705,702
        (B) FILING DATE: 23-May-1991

    (viii) ATTORNEY/AGENT INFORMATION:
        (A) NAME: Hanson, Norman D.
        (B) REGISTRATION NUMBER: 30,946
        (C) REFERENCE/DOCKET NUMBER: LUD 5253.5-US

    (ix) TELECOMMUNICATION INFORMATION:
        (A) TELEPHONE: (212)318-3168
        (B) TELEFAX: (212)752-5958

(2) INFORMATION FOR SEQUENCE ID NO: 1:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 462 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: genomic DNA
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:


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CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG AAGTTTTGCA AGTTCCGCCT ACAGCTCTAG    180
CTTGTGAATT TGTACCCTTT CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC    240
CCCCCTCCCA CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT    300
AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCCTTT GCTCTCCCAG CATGCATTGT    360
GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG CTAGCTTGCG ACTCTACTCT    420
TATCTTAACT TAGCTCGGCT TCCTGCTGGT ACCCTTTGTG CC                       462
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(2) INFORMATION FOR SEQUENCE ID NO: 2:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 675 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: genomic DNA
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:


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ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA GGT GGT     48
Met Ser Asp Asn Lys Lys Pro Asp Lys Ala His Ser Gly Ser Gly Gly
                5                  10                      15
GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG TAC TCC CTG GAA     96
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        Asp Gly Asp Gly Asn Arg Cys Asn Leu Leu His Arg Tyr Ser Leu Glu
                20                      25                  30
GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC TTC GCT GTT GTC ACA ACA           144
Glu Ile Leu Pro Tyr Leu Gly Trp Leu Val Phe Ala Val Val Thr Thr
        35                  40                  45
AGT TTT CTG GCG CTC CAG ATG TTC ATA GAC GCC CTT TAT GAG GAG CAG           192
Ser Phe Leu Ala Leu Gln Met Phe Ile Asp Ala Leu Tyr Glu Glu Gln
        50                  55                  60
TAT GAA AGG GAT GTG GCC TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC           240
Tyr Glu Arg Asp Val Ala Trp Ile Ala Arg Gln Ser Lys Arg Met Ser
65                  70                  75                  80
TCT GTC GAT GAG GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC           288
Ser Val Asp Glu Asp Glu Asp Asp Glu Asp Asp Glu Asp Asp Tyr Tyr
                85                  90                  95
GAC GAC GAG GAC GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT           336
Asp Asp Glu Asp Asp Asp Asp Asp Ala Phe Tyr Asp Asp Glu Asp Asp
            100                 105                 110
GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA GAT GAG           384
Glu Glu Glu Glu Leu Glu Asn Leu Met Asp Asp Glu Ser Glu Asp Glu
        115                 120                 125
GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA GCT GAG GAA ATG           432
Ala Glu Glu Glu Met Ser Val Glu Met Gly Ala Gly Ala Glu Glu Met
        130                 135                 140
GGT GCT GGC GCT AAC TGT GCC TGT GTT CCT GGC CAT CAT TTA AGG AAG           480
Gly Ala Gly Ala Asn Cys Ala Cys Val Pro Gly His His Leu Arg Lys
145                 150                 155                 160
AAT GAA GTG AAG TGT AGG ATG ATT TAT TTC TTC CAC GAC CCT AAT TTC           528
Asn Glu Val Lys Cys Arg Met Ile Tyr Phe Phe His Asp Pro Asn Phe
            165                 170                 175
CTG GTG TCT ATA CCA GTG AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT           576
Leu Val Ser Ile Pro Val Asn Pro Lys Glu Gln Met Glu Cys Arg Cys
            180                 185                 190
GAA AAT GCT GAT GAA GAG GTT GCA ATG GAA GAG GAA GAA GAA GAA GAG           624
Glu Asn Ala Asp Glu Glu Val Ala Met Glu Glu Glu Glu Glu Glu Glu
            195                 200                 210
GAG GAG GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC TTC TCA CCT           672
Glu Glu Glu Glu Glu Glu Glu Met Gly Asn Pro Asp Gly Phe Ser Pro
220                     225                 230                 235
TAG                                                                       675
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(2)   INFORMATION FOR SEQUENCE ID NO: 3:
        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 228 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear
        (ii) MOLECULE TYPE: genomic DNA
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

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TTCCCCTTCA TTAATTTTCT AGTTTTTAGT AATCCAGAAA ATTTGATTTT GTTCTAAAGT       120
TCATTATGCA AAGATGTCAC CAACAGACTT CTGACTGCAT GGTGAACTTT CATATGATAC       180
ATAGGATTAC ACTTGTACCT GTTAAAAATA AAAGTTTGAC TTGCATAC                    228
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(2) INFORMATION FOR SEQUENCE ID NO: 4:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1365 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: genomic DNA
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

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GAAGATCCTG ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCATCCCT         100
CAGCCAATGA GCTTACTGTT CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG         150
AAGTTTTGCA AGTTCCGCCT ACAGCTCTAG CTTGTGAATT TGTACCCTTT         200
CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC CCCCCTCCCA         250
CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT         300
AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCCTTT GCTCTCCCAG         350
CATGCATTGT GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG         400
CTAGCTTGCG ACTCTACTCT TATCTTAACT TAGCTCGGCT TCCTGCTGGT         450
ACCCTTTGTG CC                                                  462
ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA        504
GGT GGT GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG        546
TAC TCC CTG GAA GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC        588
TTC GCT GTT GTC ACA ACA AGT TTT CTG GCG CTC CAG ATG TTC        630
ATA GAC GCC CTT TAT GAG GAG CAG TAT GAA AGG GAT GTG GCC        672
TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC TCT GTC GAT GAG        714
GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC GAC GAC        756
GAG GAC GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT        798
GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA        840
GAT GAG GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA        882
GCT GAG GAA ATG GGT GCT GGC GCT AAC TGT GCC TGT GTT CCT        924
GGC CAT CAT TTA AGG AAG AAT GAA GTG AAG TGT AGG ATG ATT        966
TAT TTC TTC CAC GAC CCT AAT TTC CTG GTG TCT ATA CCA GTG       1008
AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT GAA AAT GCT GAT       1050
GAA GAG GTT GCA ATG GAA GAG GAA GAA GAA GAA GAG GAG GAG       1092
GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC TTC TCA CCT       1134
TAG                                                          1137
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ATTTGATTTT GTTCTAAAGT TCATTATGCA AAGATGTCAC CAACAGACTT        1287
CTGACTGCAT GGTGAACTTT CATATGATAC ATAGGATTAC ACTTGTACCT        1337
GTTAAAAATA AAAGTTTGAC TTGCATAC                                1365
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(2) INFORMATION FOR SEQUENCE ID NO: 5:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 4698 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

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CAGCCAATGA GCTTACTGTT CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG        150
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CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC CCCCCTCCCA        250
CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT        300
AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCCTTT GCTCTCCCAG        350
CATGCATTGT GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG        400
CTAGCTTGCG ACTCTACTCT TATCTTAACT TAGCTCGGCT TCCTGCTGGT        450
ACCCTTTGTG CC                                                 462
ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA        504
GGT GGT GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG        546
TAC TCC CTG GAA GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC        588
TTC GCT GTT GTC ACA ACA AGT TTT CTG GCG CTC CAG ATG TTC        630
ATA GAC GCC CTT TAT GAG GAG CAG TAT GAA AGG GAT GTG GCC        672
TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC TCT GTC GAT GAG        714
GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC GAC GAC        756
GAG GAC GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT        798
GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA        840
GAT GAG GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA        882
GCT GAG GAA ATG GGT GCT GGC GCT AAC TGT GCC T                 916
GTGAGTAACC CGTGGTCTTT ACTCTAGATT CAGGTGGGGT GCATTCTTTA        966
CTCTTGCCCA CATCTGTAGT AAAGACCACA TTTTGGTTGG GGGTCATTGC       1016
TGGAGCCATT CCTGGCTCTC CTGTCCACGC CTATCCCCGC TCCTCCCATC       1066
CCCCACTCCT TGCTCCGCTC TCTTTCCTTT TCCCACCTTG CCTCTGGAGC       1116
TTCAGTCCAT CCTGCTCTGC TCCCTTTCCC CTTTGCTCTC CTTGCTCCCC       1166
TCCCCCTCGG CTCAACTTTT CGTGCCTTCT GCTCTCTGAT CCCCACCCTC       1216
TTCAGGCTTC CCCATTTGCT CCTCTCCCGA AACCCTCCCC TTCCTGTTCC       1266
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TCCTGCTCCC CTCCCCCTCC CCTCCCTGTT TACCCTTCAC CGCTTTTCCT       1416
CTACCTGCTT CCCTCCCCCT TGCTGCTCCC TCCCTATTTG CATTTTCGGG       1466
TGCTCCTCCC TCCCCCTCCC CCTCCCTCCC TATTTGCATT TTCGGGTGCT       1516
CCTCCCTCCC CCTCCCCAGG CCTTTTTTTT TTTTTTTTTT TTTTTTTTTT       1566
TTGGTTTTTC GAGACAGGGT TTCTCTTTGT ATCCCTGGCT GTCCTGGCAC       1616
TCACTCTGTA GACCAGGCTG GCCTCAAACT CAGAAATCTG CCTGCCTCTG       1666
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GCCTTTCTTT TTTCTCCTCT CTGGTCTCCC TAATCCCTTT TCTGCATGTT       1766
AACTCCCCTT TTGGCACCTT TCCTTTACAG GACCCCCTCC CCCTCCCTGT       1816
TTCCCTTCCG GCACCCTTCC TAGCCCTGCT CTGTTCCCTC TCCCTGCTCC       1866
CCTCCCCCTC TTTGCTCGAC TTTTAGCAGC CTTACCTCTC CCTGCTTTCT       1916
GCCCCGTTCC CCTTTTTTGT GCCTTTCCTC CTGGCTCCCC TCCACCTTCC       1966
AGCTCACCTT TTTGTTTGTT TGGTTGTTTG GTTGTTTGGT TTGCTTTTTT       2016
TTTTTTTTTT GCACCTTGTT TTCCAAGATC CCCCTCCCCC TCCGGCTTCC       2066
CCTCTGTGTG CCTTTCCTGT TCCCTCCCCC TCGCTGGCTC CCCCTCCCTT       2116
TCTGCCTTTC CTGTCCCTGC TCCCTTCTCT GCTAACCTTT TAATGCCTTT       2166
CTTTTCTAGA CTCCCCCCTC CAGGCTTGCT GTTTGCTTCT GTGCACTTTT       2216
CCTGACCCTG CTCCCCTTCC CCTCCCAGCT CCCCCCTCTT TTCCCACCTC       2266
CCTTTCTCCA GCCTGTCACC CCTCCTTCTC TCCTCTCTGT TTCTCCCACT       2316
TCCTGCTTCC TTTACCCCTT CCCTCTCCCT ACTCTCCTCC CTGCCTGCTG       2366
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GACTTCCTCT CCAGCCGCCC AGTTCCCTGC AGTCCTGGAG TCTTTCCTGC        2416
CTCTCTGTCC ATCACTTCCC CCTAGTTTCA CTTCCCTTTC ACTCTCCCCT        2466
ATGTGTCTCT CTTCCTATCT ATCCCTTCCT TTCTGTCCCC TCTCCTCTGT        2516
CCATCACCTC TCTCCTCCCT TCCCTTTCCT CTCTCTTCCA TTTTCTTCCA        2566
CCTGCTTCTT TACCCTGCCT CTCCCATTGC CCTCTTACCT TTATGCCCAT        2616
TCCATGTCCC CTCTCAATTC CCTGTCCCAT TGTGCTCCCT CACATCTTCC        2666
ATTTCCCTCT TTCTCCCTTA GCCTCTTCTT CCTCTTCTCT TGTATCTCCC        2716
TTCCCTTTGC TTCTCCCTCC TCCTTTCCCC TTCCCCTATG CCCTCTACTC        2766
TACTTGATCT TCTCTCCTCT CCACATACCC TTTTTCCTTT CCACCCTGCC        2816
CTTTGTCCCC AGACCCTACA GTATCCTGTG CACAGGAAGT GGGAGGTGCC        2866
ATCAACAACA AGGAGGCAAG AAACAGAGCA AAATCCCAAA ATCAGCAGGA        2916
AAGGCTGGAT GAAAATAAGG CCAGGTTCTG AGGACAGCTG GAATCTAGCC        2966
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CAGGCCATGC TCCATGCTTG GCGCTTGCTC AGCGTGGTTA AGTAATGGGA        3116
GAATCTGAAA ACTAGGGGCC AGTGGTTTGT TTTGGGGACA AATTAGCACG        3166
TAGTGATATT TCCCCCTAAA AATTATAACA AACAGATTCA TGATTTGAGA        3216
TCCTTCTACA GGTGAGAAGT GGAAAAATTG TCACTATGAA GTTCTTTTTA        3266
GGCTAAAGAT ACTTGGAACC ATAGAAGCGT TGTTAAAATA CTGCTTTCTT        3316
TTGCTAAAAT ATTCTTTCTC ACATATTCAT ATTCTCCAG                    3355
 GT GTT CCT GGC CAT CAT TTA AGG AAG AAT GAA GTG AAG TGT        3396
AGG ATG ATT TAT TTC TTC CAC GAC CCT AAT TTC CTG GTG TCT        3438
ATA CCA GTG AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT GAA        3480
AAT GCT GAT GAA GAG GTT GCA ATG GAA GAG GAA GAA GAA GAA        3522
GAG GAG GAG GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC        3564
TTC TCA CCT TAG                                               3576
GCATGCAGGT ACTGGCTTCA CTAACCAACC ATTCCTAACA TATGCCTGTA        3626
GCTAAGAGCA TCTTTTTAAA AAATATTATT GGTAAACTAA ACAATTGTTA        3676
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CCCTAAGTTA AACAGAAGTC AATGATGTCT AGATGCCTGT TCTTTAGATT        3776
GTAGTGAGAC TACTTACTAC AGATGAGAAG TTGTTAGACT CGGGAGTAGA        3826
GACCAGTAAA AGATCATGCA GTGAAATGTG GCCATGGAAA TCGCATATTG        3876
TTCTTATAGT ACCTTTGAGA CAGCTGATAA CAGCTGACAA AAATAAGTGT        3926
TTCAAGAAAG ATCACACGCC ATGGTTCACA TGCAAATTAT TATTTTGTCG        3976
TTCTGATTTT TTTCATTTCT AGACCTGTGG TTTTAAAGAG ATGAAAATCT        4026
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AATGTTTTTT AAAAAAAATG CAAATCTCAT TTTTAAGAGA TGAAAGCAGA        4176
GTAACTGGGG GGCTTAGGGA ATCTGTAGGG TTGCGGTATA GCAATAGGGA        4226
GTTCTGGTCT CTGAGAAGCA GTCAGAGAGA ATGGAAAACC AGGCCCTTGC        4276
CAGTAGGTTA GTGAGGTTGA TATGATCAGA TTATGGACAC TCTCCAAATC        4326
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AGTTGCAAAG CCCAGAAGAA AGAAATGGAC AGCGGAAGAA GTGGTTGTTT        4526
TTTTTTCCCC TTCATTAATT TTCTAGTTTT TAGTAATCCA GAAAATTTGA        4576
TTTTGTTCTA AAGTTCATTA TGCAAAGATG TCACCAACAG ACTTCTGACT        4626
GCATGGTGAA CTTTCATATG ATACATAGGA TTACACTTGT ACCTGTTAAA        4676
AATAAAAGTT TGACTTGCAT AC                                      4698
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(2)   INFORMATION FOR SEQUENCE ID NO: 6:
        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 9 amino acids
            (B) TYPE: amino acid
            (D) TOPOLOGY: linear
        (ii) MOLECULE TYPE: protein
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Leu Pro Tyr Leu Gly Trp Leu Val Phe
                5

(2)   INFORMATION FOR SEQUENCE ID NO: 7:
        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 2419 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear
        (ii) MOLECULE TYPE: genomic DNA
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:


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GGATCCAGGC CCTGCCAGGA AAAATATAAG GGCCCTGCGT GAGAACAGAG          50
GGGGTCATCC ACTGCATGAG AGTGGGGATG TCACAGAGTC CAGCCCACCC         100
TCCTGGTAGC ACTGAGAAGC CAGGGCTGTG CTTGCGGTCT GCACCCTGAG         150
GGCCCGTGGA TTCCTCTTCC TGGAGCTCCA GGAACCAGGC AGTGAGGCCT         200
TGGTCTGAGA CAGTATCCTC AGGTCACAGA GCAGAGGATG CACAGGGTGT         250
GCCAGCAGTG AATGTTTGCC CTGAATGCAC ACCAAGGGCC CCACCTGCCA         300
CAGGACACAT AGGACTCCAC AGAGTCTGGC CTCACCTCCC TACTGTCAGT         350
CCTGTAGAAT CGACCTCTGC TGGCCGGCTG TACCCTGAGT ACCCTCTCAC         400
TTCCTCCTTC AGGTTTTCAG GGGACAGGCC AACCCAGAGG ACAGGATTCC         450
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TTAGAGTCTC CAAGGTTCAG TTCTCAGCTG AGGCCTCTCA CACACTCCCT         550
CTCTCCCCAG GCCTGTGGGT CTTCATTGCC CAGCTCCTGC CCACACTCCT         600
GCCTGCTGCC CTGACGAGAG TCATCATGTC TCTTGAGCAG AGGAGTCTGC         650
ACTGCAAGCC TGAGGAAGCC CTTGAGGCCC AACAAGAGGC CCTGGGCCTG         700
GTGTGTGTGC AGGCTGCCAC CTCCTCCTCC TCTCCTCTGG TCCTGGGCAC         750
CCTGGAGGAG GTGCCCACTG CTGGGTCAAC AGATCCTCCC CAGAGTCCTC         800
AGGGAGCCTC CGCCTTTCCC ACTACCATCA ACTTCACTCG ACAGAGGCAA         850
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GCAGAAATGC TGGAGAGTGT CATCAAAAAT TACAAGCACT GTTTTCCTGA        1050
GATCTTCGGC AAAGCCTCTG AGTCCTTGCA GCTGGTCTTT GGCATTGACG        1100
TGAAGGAAGC AGACCCCACC GGCCACTCCT ATGTCCTTGT CACCTGCCTA        1150
GGTCTCTCCT ATGATGGCCT GCTGGGTGAT AATCAGATCA TGCCCAAGAC        1200
AGGCTTCCTG ATAATTGTCC TGGTCATGAT TGCAATGGAG GGCGGCCATG        1250
CTCCTGAGGA GGAAATCTGG GAGGAGCTGA GTGTGATGGA GGTGTATGAT        1300
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ACCTTCCAGG GCCGCGTCCA GCAGCTTCCC CTGCCTCGTG TGACATGAGG        1650
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TCAAATGTTT TTTTTAAGG DATGGTTGAA TGAACTTCAG CATCCAAGTT        1800
TATGAATGAC AGCAGTCACA CAGTTCTGTG TATATAGTTT AAGGGTAAGA        1850
GTCTTGTGTT TTATTCAGAT TGGGAAATCC ATTCTATTTT GTGAATTGGG        1900
ATAATAACAG CAGTGGAATA AGTACTTAGA AATGTGAAAA ATGAGCAGTA        1950
AAATAGATGA GATAAAGAAC TAAAGAAATT AAGAGATAGT CAATTCTTGC        2000
CTTATACCTC AGTCTATTCT GTAAAATTTT TAAAGATATA TGCATACCTG        2050
GATTTCCTTG GCTTCTTTGA GAATGTAAGA GAAATTAAAT CTGAATAAAG        2100
AATTCTTCCT GTTCACTGGC TCTTTTCTTC TCCATGCACT GAGCATCTGC        2150
TTTTTGGAAG GCCCTGGGTT AGTAGTGGAG ATGCTAAGGT AAGCCAGACT        2200
CATACCCACC CATAGGGTCG TAGAGTCTAG GAGCTGCAGT CACGTAATCG        2250
AGGTGGCAAG ATGTCCTCTA AAGATGTAGG GAAAAGTGAG AGAGGGGTGA        2300
GGGTGTGGGG CTCCGGGTGA GAGTGGTGGA GTGTCAATGC CCTGAGCTGG        2350
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AATGATCTTG GGTGGATCC                                          2419
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(2)   INFORMATION FOR SEQUENCE ID NO: 8:
      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 5674 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear
      (ii) MOLECULE TYPE: genomic DNA
      (ix) FEATURE:
           (A) NAME/KEY: MAGE-1 gene
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

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AGAATCCGGT TCCACCCCTG CTCTCAACCC AGGGAAGCCC AGGTGCCCAG          150
ATGTGACGCC ACTGACTTGA GCATTAGTGG TTAGAGAGAA GCGAGGTTTT          200
CGGTCTGAGG GGCGGCTTGA GATCGGTGGA GGGAAGCGGG CCCAGCTCTG          250
TAAGGAGGCA AGGTGACATG CTGAGGGAGG ACTGAGGACC CACTTACCCC          300
AGATAGAGGA CCCCAAATAA TCCCTTCATG CCAGTCCTGG ACCATCTGGT          350
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CTGGGGACTC GAAGTCAGAG CTCCGTGTGA TCAGGGAAGG GCTGCTTAGG          450
AGAGGGCAGC GTCCAGGCTC TGCCAGACAT CATGCTCAGG ATTCTCAAGG          500
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ATGCTCACTC CCGTGACCCA ACCCCCTCTT CATTGTCATT CCAACCCCCA          600
CCCCACATCC CCCACCCCAT CCCTCAACCC TGATGCCCAT CCGCCCAGCC          650
ATTCCACCCT CACCCCCACC CCCACCCCCA CGCCCACTCC CACCCCCACC          700
CAGGCAGGAT CCGGTTCCCG CCAGGAAACA TCCGGGTGCC CGGATGTGAC          750
GCCACTGACT TGCGCATTGT GGGGCAGAGA GAAGCGAGGT TTCCATTCTG          800
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CGCGGGAAGA CGTCTCAGCC TGGGCTGCCC CCAGACCCCT GCTCCAAAAG       1000
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TGTGACCAGG GCAGGACTGG TTAGGAGAGG GCAGGGCACA GGCTCTGCCA       1100
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CCTGACCACC ACCCTCCAGC CCCAGCACCA GCCCCAACCC TTCTGCCACC       1300
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ATCCAGTACC ACCCCTGCTG CCAGCCCTGG ACCACCCGGC CAGGACAGAT       1650
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CAGGACACAT TAATTCCAAT GAATTTTGAT ATCTCTTGCT GCCCTTCCCC       3150
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CAGAGGGGGT CATCCACTGC ATGAGAGTGG GGATGTCACA GAGTCCAGCC       3350
CACCCTCCTG GTAGCACTGA GAAGCCAGGG CTGTGCTTGC GGTCTGCACC       3400
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GCC CTT GAG GCC CAA CAA GAG GCC CTG GGC CTG GTG TGT GTG          3964
CAG GCT GCC ACC TCC TCC TCC TCT CCT CTG GTC CTG GGC ACC          4006
CTG GAG GAG GTG CCC ACT GCT GGG TCA ACA GAT CCT CCC CAG          4048
AGT CCT CAG GGA GCC TCC GCC TTT CCC ACT ACC ATC AAC TTC          4090
ACT CGA CAG AGG CAA CCC AGT GAG GGT TCC AGC AGC CGT GAA          4132
GAG GAG GGG CCA AGC ACC TCT TGT ATC CTG AGT CCT TGT TTC          4184
CGA GCA GTA ATC ACT AAG AAG GTG GCT GAT TTG GTT GGT TTT          4216
CTG CTC CTC AAA TAT CGA GCC AGG GAG CCA GTC ACA AAG GCA          4258
GAA ATG CTG GAG AGT GTC ATC AAA AAT TAC AAG CAC TGT TTT          4300
CCT GAG ATC TTC GGC AAA GCC TCT GAG TCC TTG CAG CTG GTC          4342
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CTG GGT GAT AAT CAG ATC ATG CCC AAG ACA GGC TTC CTG ATA          4468
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GGTGAGGGTG TGGGGCTCCG GGTGAGAGTG GTGGAGTGTC AATGCCCTGA          5600
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(2) INFORMATION FOR SEQUENCE ID NO: 9:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 4157 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: genomic DNA
    (ix) FEATURE:
        (A) NAME/KEY: MAGE-2 gene
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:


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GAGGGAAGCA GGCGCAGGCT CCGTGAGGAG GCAAGGTAAG ACGCCGAGGG        200
AGGACTGAGG CGGGCCTCAC CCCAGACAGA GGGCCCCCAA TTAATCCAGC        250
GCTGCCTCTG CTGCCGGGCC TGGACCACCC TGCAGGGGAA GACTTCTCAG        300
GCTCAGTCGC CACCACCTCA CCCCGCCACC CCCGCCGCT TTAACCGCAG         350
GGAACTCTGG CGTAAGAGCT TTGTGTGACC AGGGCAGGGC TGGTTAGAAG        400
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GACTGAGGGC AACCCACCCC CTACCCTCAC TACCAATCCC ATCCCCCAAC        500
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TCCCATCTCC TCCCCCACCA CCATCCTGGC AGAATCCGGC TTTGCCCCTG        600
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ACGTTCACAT GTACGGCTAA GGGAGGGAAG GGGTTGGGTC TCGTGAGTAT        700
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TCCTTAGGGG ACCCAGCATG CCAGGACAGG GGGCCCACTG TACCCCTGTC        800
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576670.1

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GAC TCA CCG AGT CCT CCC CAC AGT CCT CAG GGA GCC TCC AGC     2807
TTC TCG ACT ACC ATC AAC TAC ACT CTT TGG AGA CAA TCC GAT     2849
GAG GGC TCC AGC AAC CAA GAA GAG GAG GGG CCA AGA ATG TTT     2891
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GGC CTC TCC TAC GAT GGC CTG CTG GGC GAC AAT CAG GTC ATG     3185
CCC AAG ACA GGC CTC CTG ATA ATC GTC CTG GCC ATA ATC GCA     3227
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GGA GAA CCT CAC ATT TCC TAC CCA CCC CTG CAT GAA CGG GCT     3521
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(2) INFORMATION FOR SEQUENCE ID NO: 10:
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          (A) LENGTH: 662 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: genomic DNA
     (ix) FEATURE:
          (A) NAME/KEY: MAGE-21 gene
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

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(2) INFORMATION FOR SEQUENCE ID NO: 11:
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          (A) LENGTH: 1640 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA to mRNA
     (ix) FEATURE:
          (A) NAME/KEY: cDNA MAGE-3
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

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GTTGCCCTGA CCAGAGTCAT C   171
ATG CCT CTT GAG CAG AGG AGT CAG CAC TGC AAG CCT GAA GAA   213
GGC CTT GAG GCC CGA GGA GAG GCC CTG GGC CTG GTG GGT GCG   255
CAG GCT CCT GCT ACT GAG GAG CAG GAG GCT GCC TCC TCC TCT   297
TCT ACT CTA GTT GAA GTC ACC CTG GGG GAG GTG CCT GCT GCC   339
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576670.1

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AGG GAG CCG GTC ACA AAG GCA GAA ATG CTG GGG AGT GTC GTC                   591
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(2)   INFORMATION FOR SEQUENCE ID NO: 12:
       (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 943 base pairs
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: single
              (D) TOPOLOGY: linear
       (ii) MOLECULE TYPE: genomic DNA
       (ix) FEATURE:
              (A) NAME/KEY: MAGE-31 gene
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

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GATAGTGCCA ACGGTGAAGG TTTGCCTTGG ATTCAAACCA AGGGCCCCAC                   250
CTGCCCCAGA ACACATGGAC TCCAGAGCGC CTGGCCTCAC CCTCAATACT                   300
TTCAGTCCTG CAGCCTCAGC ATGCGCTGGC CGGATGTACC CTGAGGTGCC                   350
CTCTCACTTC CTCCTTCAGG TTCTGAGGGG ACAGGCTGAC CTGGAGGACC                   400
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CTCCCGCCTG TTGCCCTGAC CAGAGTCATC                                   580
ATG CCT CTT GAG CAG AGG AGT CAG CAC TGC AAG CCT GAA GAA            622
GGC CTT GAG GCC CGA GGA GAg GCC CTG GGC CTG GTG GGT GCG            664
CAG GCT CCT GCT ACT GAG GAG CAG GAG GCT GCC TCC TCC TCT           706
TCT AGT GTA GTT GAA GTC ACC CTG GGG GAG GTG CCT GCT GCC           748
GAG TCA CCA GAT CCT CCC CAG AGT CCT CAG GGA GCC TCC AGC           790
CTC CCC ACT ACC ATG AAC TAC CCT CTC TGG AGC CAA TCC TAT           832
GAG GAC TCC AGC AAC CAA GAA GAG GAG GGG CCA AGC ACC TTC           874
CCT GAC CTG GAG TCT GAG TTC CAA GCA GCA CTC AGT AGG AAG           916
GTG GCC AAG TTG GTT CAT TTT CTG CTC                                943


        (2)    INFORMATION FOR SEQUENCE ID NO: 13:
               (i)  SEQUENCE CHARACTERISTICS:
                      (A)  LENGTH:   2531 base pairs
                      (B)  TYPE:    nucleic acid
                      (C)  STRANDEDNESS: single
                      (D)  TOPOLOGY:   linear
               (ii) MOLECULE TYPE:  genomic DNA
               (ix) FEATURE:
                      (A)  NAME/KEY:   MAGE-4 gene
               (xi) SEQUENCE DESCRIPTION:   SEQ ID NO: 13:


GGATCCAGGC CCTGCCTGGA GAAATGTGAG GGCCCTGAGT GAACACAGTG             50
GGGATCATCC ACTCCATGAG AGTGGGGACC TCACAGAGTC CAGCCTACCC            100
TCTTGATGGC ACTGAGGGAC CGGGGCTGTG CTTACAGTCT GCACCCTAAG            150
GGCCCATGGA TTCCTCTCCT AGGAGCTCCA GGAACAAGGC AGTGAGGCCT            200
TGGTCTGAGA CAGTGTCCTC AGGTTACAGA GCAGAGGATG CACAGGCTGT            250
GCCAGCAGTG AATGTTTGCC CTGAATGCAC ACCAAGGGCC CCACCTGCCA            300
CAAGACACAT AGGACTCCAA AGAGTCTGGC CTCACCTCCC TACCATCAAT            350
CCTGCAGAAT CGACCTCTGC TGGCCGGCTA TACCCTGAGG TGCTCTCTCA            400
CTTCCTCCTT CAGGTTCTGA GCAGACAGGC CAACCGGAGA CAGGATTCCC            450
TGGAGGCCAC AGAGGAGCAC CAAGGAGAAG ATCTGTAAGT AAGCCTTTGT            500
TAGAGCCTCT AAGATTTGGT TCTCAGCTGA GGTCTCTCAC ATGCTCCCTC            550
TCTCCGTAGG CCTGTGGGTC CCCATTGCCC AGCTTTTGCC TGCACTCTTG            600
CCTGCTGCCC TGACCAGAGT CATC                                         624
ATG TCT TCT GAG CAG AAG AGT CAG CAC TGC AAG CCT GAG GAA            666
GGC GTT GAG GCC CAA GAA GAG GCC CTG GGC CTG GTG GGT GCA            708
CAG GCT CCT ACT ACT GAG GAG CAG GAG GCT GCT GTC TCC TCC            750
TCC TCT CCT CTG GTC CCT GGC ACC CTG GAG GAA GTG CCT GCT           792
GCT GAG TCA GCA GGT CCT CCC CAG AGT CCT CAG GGA GCC TCT           834
GCC TTA CCC ACT ACC ATC AGC TTC ACT TGC TGG AGG CAA CCC           876
AAT GAG GGT TCC AGC AGC CAA GAA GAG GAG GGG CCA AGC ACC            918
TCG CCT GAC GCA GAG TCC TTG TTC CGA GAA GCA CTC AGT AAC           960
AAG GTG GAT GAG TTG GCT CAT TTT CTG CTC CGC AAG TAT CGA          1002
GCC AAG GAG CTG GTC ACA AAG GCA GAA ATG CTG GAG AGA GTC          1044
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ATC AAA AAT TAC AAG CGC TGC TTT CCT GTG ATC TTC GGC AAA          1086
GCC TCC GAG TCC CTG AAG ATG ATC TTT GGC ATT GAC GTG AAG          1128
GAA GTG GAC CCC GCC AGC AAC ACC TAC ACC CTT GTC ACC TGC          1170
CTG GGC CTT TCC TAT GAT GGC CTG CTG GGT AAT AAT CAG ATC          1212
TTT CCC AAG ACA GGC CTT CTG ATA ATC GTC CTG GGC ACA ATT          1254
GCA ATG GAG GGC GAC AGC GCC TCT GAG GAG GAA ATC TGG GAG          1296
GAG CTG GGT GTG ATG GGG GTG TAT GAT GGG AGG GAG CAC ACT          1338
GTC TAT GGG GAG CCC AGG AAA CTG CTC ACC CAA GAT TGG GTG          1380
CAG GAA AAC TAC CTG GAG TAC CGG CAG GTA CCC GGC AGT AAT          1422
CCT GCG CGC TAT GAG TTC CTG TGG GGT CCA AGG GCT CTG GCT          1464
GAA ACC AGC TAT GTG AAA GTC CTG GAG CAT GTG GTC AGG GTC          1506
AAT GCA AGA GTT CGC ATT GCC TAC CCA TCC CTG CGT GAA GCA          1548
GCT TTG TTA GAG GAG GAA GAG GGA GTC TGA                          1578
GCATGAGTTG CAGCCAGGGC TGTGGGGAAG GGGCAGGGCT GGGCCAGTGC           1628
ATCTAACAGC CCTGTGCAGC AGCTTCCCTT GCCTCGTGTA ACATGAGGCC           1678
CATTCTTCAC TCTGTTTGAA GAAAATAGTC AGTGTTCTTA GTAGTGGGTT           1728
TCTATTTTGT TGGATGACTT GGAGATTTAT CTCTGTTTCC TTTTACAATT           1778
GTTGAAATGT TCCTTTTAAT GGATGGTTGA ATTAACTTCA GCATCCAAGT           1828
TTATGAATCG TAGTTAACGT ATATTGCTGT TAATATAGTT TAGGAGTAAG           1878
AGTCTTGTTT TTTATTCAGA TTGGGAAATC CGTTCTATTT TGTGAATTTG           1928
GGACATAATA ACAGCAGTGG AGTAAGTATT TAGAAGTGTG AATTCACCGT           1978
GAAATAGGTG AGATAAATTA AAAGATACTT AATTCCCGCC TTATGCCTCA           2028
GTCTATTCTG TAAAATTTAA AAATATATAT GCATACCTGG ATTTCCTTGG           2078
CTTCGTGAAT GTAAGAGAAA TTAAATCTGA ATAAATAATT CTTTCTGTTA           2128
ACTGGCTCAT TTCTTCTCTA TGCACTGAGC ATCTGCTCTG TGGAAGGCCC           2178
AGGATTAGTA GTGGAGATAC TAGGGTAAGC CAGACACACA CCTACCGATA           2228
GGGTATTAAG AGTCTAGGAG CGCGGTCATA TAATTAAGGT GACAAGATGT           2278
CCTCTAAGAT GTAGGGGAAA AGTAACGAGT GTGGGTATGG GGCTCCAGGT           2328
GAGAGTGGTC GGGTGTAAAT TCCCTGTGTG GGGCCTTTTG GGCTTTGGGA           2378
AACTGCATTT TCTTCTGAGG GATCTGATTC TAATGAAGCT TGGTGGGTCC           2428
AGGGCCAGAT TCTCAGAGGG AGAGGGAAAA GCCCAGATTG GAAAAGTTGC           2478
TCTGAGCAGT TCCTTTGTGA CAATGGATGA ACAGAGAGGA GCCTCTACCT           2528
GGG                                                             2531
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(2)   INFORMATION FOR SEQUENCE ID NO: 14:
       (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 2531 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS:single
            (D) TOPOLOGY: linear
       (ii) MOLECULE TYPE: genomic DNA
       (ix) FEATURE:
            (A) NAME/KEY: MAGE-41 gene
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:


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GGATCCAGGC CCTGCCTGGA GAAATGTGAG GGCCCTGAGT GAACACAGTG            50
GGGATCATCC ACTCCATGAG AGTGGGGACC TCACAGAGTC CAGCCTACCC           100
TCTTGATGGC ACTGAGGGAC CGGGGCTGTG CTTACAGTCT GCACCCTAAG           150
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GGCCCATGGA TTCCTCTCCT AGGAGCTCCA GGAACAAGGC AGTGAGGCCT        200
TGGTCTGAGA CAGTGTCCTC AGGTTACAGA GCAGAGGATG CACAGGCTGT        250
GCCAGCAGTG AATGTTTGCC CTGAATGCAC ACCAAGGGCC CCACCTGCCA        300
CAAGACACAT AGGACTCCAA AGAGTCTGGC CTCACCTCCC TACCATCAAT        350
CCTGCAGAAT CGACCTCTGC TGGCCGGCTA TACCCTGAGG TGCTCTCTCA        400
CTTCCTCCTT CAGGTTCTGA GCAGACAGGC CAACCGGAGA CAGGATTCCC        450
TGGAGGCCAC AGAGGAGCAC CAAGGAGAAG ATCTGTAAGT AAGCCTTTGT        500
TAGAGCCTCT AAGATTTGGT TCTCAGCTGA GGTCTCTCAC ATGCTCCCTC        550
TCTCCGTAGG CCTGTGGGTC CCCATTGCCC AGCTTTTGCC TGCACTCTTG        600
CCTGCTGCCC TGAGCAGAGT CATC                                    624
ATG TCT TCT GAG CAG AAG AGT CAG CAC TGC AAG CCT GAG GAA        666
GGC GTT GAG GCC CAA GAA GAG GCC CTG GGC CTG GTG GGT GCG        708
CAG GCT CCT ACT ACT GAG GAG CAG GAG GCT GCT GTC TCC TCC        750
TCC TCT CCT CTG GTC CCT GGC ACC CTG GAG GAA GTG CCT GCT        792
GCT GAG TCA GCA GGT CCT CCC CAG AGT CCT CAG GGA GCC TCT        834
GCC TTA CCC ACT ACC ATC AGC TTC ACT TGC TGG AGG CAA CCC        876
AAT GAG GGT TCC AGC AGC CAA GAA GAG GAG GGG CCA AGC ACC        918
TCG CCT GAC GCA GAG TCC TTG TTC CGA GAA GCA CTC AGT AAC        960
AAG GTG GAT GAG TTG GCT CAT TTT CTG CTC CGC AAG TAT CGA        1002
GCC AAG GAG CTG GTC ACA AAG GCA GAA ATG CTG GAG AGA GTC        1044
ATC AAA AAT TAC AAG CGC TGC TTT CCT GTG ATC TTC GGC AAA        1086
GCC TCC GAG TCC CTG AAG ATG ATC TTT GGC ATT GAC GTG AAG        1128
GAA GTG GAC CCC ACC AGC AAC ACC TAC ACC CTT GTC ACC TGC        1170
CTG GGC CTT TCC TAT GAT GGC CTG CTG GGT AAT AAT CAG ATC        1212
TTT CCC AAG ACA GGC CTT CTG ATA ATC GTC CTG GGC ACA ATT        1254
GCA ATG GAG GGC GAC AGC GCC TCT GAG GAG GAA ATC TGG GAG        1296
GAG CTG GGT GTG ATG GGG GTG TAT GAT GGG AGG GAG CAC ACT        1338
GTC TAT GGG GAG CCC AGG AAA CTG CTC ACC CAA GAT TGG GTG        1380
CAG GAA AAC TAC CTG GAG TAC CGG CAG GTA CCC GGC AGT AAT        1422
CCT GCG CGC TAT GAG TTC CTG TGG GGT CCA AGG GCT CTG GCT        1464
GAA ACC AGC TAT GTG AAA GTC CTG GAG CAT GTG GTC AGG GTC        1506
AAT GCA AGA GTT CGC ATT GCC TAC CCA TCC CTG CGT GAA GCA        1548
GCT TTG TTA GAG GAG GAA GAG GGA GTC TGA                       1578
GCATGAGTTG CAGCCAGGGC TGTGGGGAAG GGGCAGGGCT GGGCCAGTGC        1628
ATCTAACAGC CCTGTGCAGC AGCTTCCCTT GCCTCGTGTA ACATGAGGCC        1678
CATTCTTCAC TCTGTTTGAA GAAAATAGTC AGTGTTCTTA GTAGTGGGTT        1728
TCTATTTTGT TGGATGACTT GGAGATTTAT CTCTGTTTCC TTTTACAATT        1778
GTTGAAATGT TCCTTTTAAT GGATGGTTGA ATTAACTTCA GCATCCAAGT        1828
TTATGAATCG TAGTTAACGT ATATTGCTGT TAATATAGTT TAGGAGTAAG        1878
AGTCTTGTTT TTTATTCAGA TTGGGAAATC CGTTCTATTT TGTGAATTTG        1928
GGACATAATA ACAGCAGTGG AGTAAGTATT TAGAAGTGTG AATTCACCGT        1978
GAAATAGGTG AGATAAATTA AAAGATACTT AATTCCCGCC TTATGCCTCA        2028
GTCTATTCTG TAAAATTTAA AAATATATAT GCATACCTGG ATTTCCTTGG        2078
CTTCGTGAAT GTAAGAGAAA TTAAATCTGA ATAAATAATT CTTTCTGTTA        2128
ACTGGCTCAT TTCTTCTCTA TGCACTGAGC ATCTGCTCTG TGGAAGGCCC        2178
AGGATTAGTA GTGGAGATAC TAGGGTAAGC CAGACACACA CCTACCGATA        2228
GGGTATTAAG AGTCTAGGAG CGCGGTCATA TAATTAAGGT GACAAGATGT        2278
CCTCTAAGAT GTAGGGGAAA AGTAACGAGT GTGGGTATGG GGCTCCAGGT        2328
GAGAGTGGTC GGGTGTAAAT TCCCTGTGTG GGGCCTTTTG GGCTTTGGGA        2378
AACTCCATTT TCTTCTGAGG GATCTGATTC TAATGAAGCT TGGTGGGTCC        2428
AGGGCCAGAT TCTCAGAGGG AGAGGGAAAA GCCCAGATTG GAAAAGTTGC        2478
TCTGAGCGGT TCCTTTGTGA CAATGGATGA ACAGAGAGGA GCCTCTACCT        2528
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(2)   INFORMATION FOR SEQUENCE ID NO: 15:
       (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 1068 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear
       (ii) MOLECULE TYPE: cDNA to mRNA
       (ix) FEATURE:
           (A) NAME/KEY: cDNA MAGE-4
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

  G GGG CCA AGC ACC TCG CCT GAC GCA GAG TCC TTG TTC CGA   40
GAA GCA CTC AGT AAC AAG GTG GAT GAG TTG GCT CAT TTT CTG   82
CTC CGC AAG TAT CGA GCC AAG GAG CTG GTC ACA AAG GCA GAA   124
ATG CTG GAG AGA GTC ATC AAA AAT TAC AAG CGC TGC TTT CCT   166
GTG ATC TTC GGC AAA GCC TCC GAG TCC CTG AAG ATG ATC TTT   208
GGC ATT GAC GTG AAG GAA GTG GAC CCC GCC AGC AAC ACC TAC   250
ACC CTT GTC ACC TGC CTG GGC CTT TCC TAT GAT GGC CTG CTG   292
GGT AAT AAT CAG ATC TTT CCC AAG ACA GGC CTT CTG ATA ATC   334
GTC CTG GGC ACA ATT GCA ATG GAG GGC GAC AGC GCC TCT GAG   376
GAG GAA ATC TGG GAG GAG CTG GGT GTG ATG GGG GTG TAT GAT   418
GGG AGG GAG CAC ACT GTC TAT GGG GAG CCC AGG AAA CTG CTC   460
ACC CAA GAT TGG GTG CAG GAA AAC TAC CTG GAG TAC CGG CAG   502
GTA CCC GGC AGT AAT CCT GCG CGC TAT GAG TTC CTG TGG GGT   544
CCA AGG GCT CTG GCT GAA ACC AGC TAT GTG AAA GTC CTG GAG   586
CAT GTG GTC AGG GTC AAT GCA AGA GTT CGC ATT GCC TAC CCA   628
TCC CTG CGT GAA GCA GCT TTG TTA GAG GAG GAA GAG GGA GTC   670
TGAGCATGAG TTGCAGCCAG GGCTGTGGGG AAGGGGCAGG GCTGGGCCAG   720
TGCATCTAAC AGCCCTGTGC AGCAGCTTCC CTTGCCTCGT GTAACATGAG   770
GCCCATTCTT CACTCTGTTT GAAGAAAATA GTCAGTGTTC TTAGTAGTGG   820
GTTTCTATTT TGTTGGATGA CTTGGAGATT TATCTCTGTT TCCTTTTACA   870
ATTGTTGAAA TGTTCCTTTT AATGGATGGT TGAATTAACT TCAGCATCCA   920
AGTTTATGAA TCGTAGTTAA CGTATATTGC TGTTAATATA GTTTAGGAGT   970
AAGAGTCTTG TTTTTTATTC AGATTGGGAA ATCCGTTCTA TTTTGTGAAT   1020
TTGGGACATA ATAACAGCAG TGGAGTAAGT ATTTAGAAGT GTGAATTC   1068

(2)   INFORMATION FOR SEQUENCE ID NO: 16:
       (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 2226 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear
       (ii) MOLECULE TYPE: genomic DNA
       (ix) FEATURE:
           (A) NAME/KEY: MAGE-5 gene
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

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GGGACCATTC ACCCCAAGAG GGTGGAGACC TCACAGATTC CAGCCTACCC     100
TCCTGTTAGC ACTGGGGGCC TGAGGCTGTG CTTGCAGTCT GCACCCTGAG     150
GGCCCATGCA TTCCTCTTCC AGGAGCTCCA GGAAACAGAC ACTGAGGCCT     200
TGGTCTGAGG CCGTGCCCTC AGGTCACAGA GCAGAGGAGA TGCAGACGTC     250
TAGTGCCAGC AGTGAACGTT TGCCTTGAAT GCACACTAAT GGCCCCCATC     300
GCCCCAGAAC ATATGGGACT CCAGAGCACC TGGCCTCACC CTCTCTACTG     350
TCAGTCCTGC AGAATCAGCC TCTGCTTGCT TGTGTACCCT GAGGTGCCCT     400
CTCACTTTTT CCTTCAGGTT CTCAGGGGAC AGGCTGACCA GGATCACCAG     450
GAAGCTCCAG AGGATCCCCA GGAGGCCCTA GAGGAGCACC AAAGGAGAAG     500
ATCTGTAAGT AAGCCTTTGT TAGAGCCTCC AAGGTTCAGT TTTTAGCTGA     550
GGCTTCTCAC ATGCTCCCTC TCTCTCCAGG CCAGTGGGTC TCCATTGCCC     600
AGCTCCTGCC CACACTCCTG CCTGTTGCGG TGACCAGAGT CGTC          644
ATG TCT CTT GAG CAG AAG AGT CAG CAC TGC AAG CCT GAG GAA      686
CTC CTC TGG TCC CAG GCA CCC TGG GGG AGG TGC CTG CTG CTG      728
GGT CAC CAG GTC CTC TCA AGA GTC CTC AGG GAG CCT CCG CCA      770
TCC CCA CTG CCA TCG ATT TCA CTC TAT GGA GGC AAT CCA TTA      812
AGG GCT CCA GCA ACC AAG AAG AGG AGG GGC CAA GCA CCT CCC      854
CTG ACC CAG AGT CTG TGT TCC GAG CAG CAC TCA GTA AGA AGG      896
TGG CTG ACT TGA                                             908
TTCATTTTCT GCTCCTCAAG TATTAAGTCA AGGAGCTGGT CACAAAGGCA     958
GAAATGCTGG AGAGCGTCAT CAAAAATTAC AAGCGCTGCT TTCCTGAGAT    1008
CTTCGGCAAA GCCTCCGAGT CCTTGCAGCT GGTCTTTGGC ATTGACGTGA    1058
AGGAAGCGGA CCCCACCAGC AACACCTACA CCCTTGTCAC CTGCCTGGGA    1108
CTCCTATGAT GGCCTGCTGG TTGATAATAA TCAGATCATG CCCAAGACGG    1158
GCCTCCTGAT AATCGTCTTG GGCATGATTG CAATGGAGGG CAAATGCGTC    1208
CCTGAGGAGA AAATCTGGGA GGAGCTGAGT GTGATGAAGG TGTATGTTGG    1258
GAGGGAGCAC AGTGTCTGTG GGGAGCCCAG GAAGCTGCTC ACCCAAGATT    1308
TGGTGCAGGA AAACTACCTG GAGTACCGGC AGGTGCCCAG CAGTGATCCC    1358
ATATGCTATG AGTTACTGTG GGGTCCAAGG GCACTCGCTG CTTGAAAGTA    1408
CTGGAGCACG TGGTCAGGGT CAATGCAAGA GTTCTCATTT CCTACCCATC    1458
CCTGCGTGAA GCAGCTTTGA GAGAGGAGGA AGAGGGAGTC TGAGCATGAG    1508
CTGCAGCCAG GGCCACTGCG AGGGGGGCTG GGCCAGTGCA CCTTCCAGGG    1558
CTCCGTCCAG TAGTTTCCCC TGCCTTAATG TGACATGAGG CCCATTCTTC    1608
TCTCTTTGAA GAGAGCAGTC AACATTCTTA GTAGTGGGTT TCTGTTCTAT    1658
TGGATGACTT TGAGATTTGT CTTTGTTTCC TTTTGGAATT GTTCAAATGT    1708
TTCTTTTAAT GGGTGGTTGA ATGAACTTCA GCATTCAAAT TTATGAATGA    1758
CAGTAGTCAC ACATAGTGCT GTTTATATAG TTTAGGAGTA AGAGTCTTGT    1808
TTTTTATTCA GATTGGGAAA TCCATTCCAT TTTGTGAATT GGGACATAGT    1858
TACAGCAGTG AATAAGTAT TCATTAGAA ATGTGAATGA GCAGTAAAAC    1908
TGATGACATA AAGAAATTAA AAGATATTTA ATTCTTGCTT ATACTCAGTC    1958
TATTCGGTAA AATTTTTTTT AAAAAATGTG CATACCTGGA TTTCCTTGGC    2008
TTCTTTGAGA ATGTAAGACA AATTAAATCT GAATAAATCA TTCTCCCTGT    2058
TCACTGGCTC ATTTATTCTC TATGCACTGA GCATTTGCTC TGTGGAAGGC    2108
CCTGGGTTAA TAGTGGAGAT GCTAAGGTAA GCCAGACTCA CCCCTACCCA    2158
CAGGGTAGTA AAGTCTAGGA GCAGCAGTCA TATAATTAAG GTGGAGAGAT    2208
GCCCTCTAAG ATGTAGAG                                       2226
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GGATCCAGGC CTTGCCAGGA GAAAGGTGAG GGCCCTGTGT GAGCACAGAG        50
GGGACCATTC ACCCCAAGAG GGTGGAGACC TCACAGATTC CAGCCTACCC       100
TCCTGTTAGC ACTGGGGGCC TGAGGCTGTG CTTGCAGTCT GCACCCTGAG       150
GGCCCATGCA TTCCTCTTCC AGGAGCTCCA GGAAACAGAC ACTGAGGCCT       200
TGGTCTGAGG CCGTGCCCTC AGGTCACAGA GCAGAGGAGA TGCAGACGTC       250
TAGTGCCAGC AGTGAACGTT TGCCTTGAAT GCACACTAAT GGCCCCCATC       300
GCCCCAGAAC ATATGGGACT CCAGAGCACC TGGCCTCACC CTCTCTACTG       350
TCAGTCCTGC AGAATCAGCC TCTGCTTGCT TGTGTACCCT GAGGTGCCCT       400
CTCACTTTTT CCTTCAGGTT CTCAGGGGAC AGGCTGACCA GGATCACCAG       450
GAAGCTCCAG AGGATCCCCA GGAGGCCCTA GAGGAGCACC AAAGGAGAAG       500
ATCTGTAAGT AAGCCTTTGT TAGAGCCTCC AAGGTTCAGT TTTTAGCTGA       550
GGCTTCTCAC ATGCTCCCTC TCTCTCCAGG CCAGTGGGTC TCCATTGCCC       600
AGCTCCTGCC CACACTCCTG CCTGTTGCGG TGACCAGAGT CGTC            644
ATG TCT CTT GAG CAG AAG AGT CAG CAC TGC AAG CCT GAG GAA       686
GGC CTT GAC ACC CAA GAA GAG CCC TGG GCC TGG TGG GTG TGC       728
AGG CTG CCA CTA CTG AGG AGC AGG AGG CTG TGT CCT CCT CCT       770
CTC CTC TGG TCC CAG GCA CCC TGG GGG AGG TGC CTG CTG CTG       812
GGT CAC CAG GTC CTC TCA AGA GTC CTC AGG GAG CCT CCG CCA       854
TCC CCA CTG CCA TCG ATT TCA CTC TAT GGA GGC AAT CCA TTA       896
AGG GCT CCA GCA ACC AAG AAG AGG AGG GGC CAA GCA CCT CCC       938
CTG ACC CAG AGT CTG TGT TCC GAG CAG CAC TCA GTA AGA AGG       980
TGG CTG ACT TGA                                              992
TTCATTTTCT GCTCCTCAAG TATTAAGTCA AGGAGCCGGT CACAAAGGCA      1042
GAAATGCTGG AGAGCGTCAT CAAAAATTAC AAGCGCTGCT TCCTGAGAT       1092
CTTCGGCAAA GCCTCCGAGT CCTTGCAGCT GGTCTTTGGC ATTGACGTGA      1142
AGGAAGCGGA CCCCACCAGC AACACCTACA CCCTTGTCAC CTGCCTGGGA      1192
CTCCTATGAT GGCCTGGTGG TTTAATCAGA TCATGCCCAA GACGGGCCTC      1242
CTGATAATCG TCTTGGGCAT GATTGCAATG GAGGGCAAAT GCGTCCCTGA      1292
GGAGAAAATC TGGGAGGAGC TGGGTGTGAT GAAGGTGTAT GTTGGGAGGG      1342
AGCACAGTGT CTGTGGGGAG CCCAGGAAGC TGCTCACCCA AGATTTGGTG      1392
CAGGAAAACT ACCTGGAGTA CCGCAGGTGC CCAGCAGTGA TCCCATATGC      1442
TATGAGTTAC TGTGGGGTCC AAGGGCACTC GCTGCTTGAA AGTACTGGAG      1492
CACGTGGTCA GGGTCAATGC AAGAGTTCTC ATTTCCTACC CATCCCTGCA      1542
TGAAGCAGCT TTGAGAGAGG AGGAAGAGGG AGTCTGAGCA TGAGCTGCAG      1592
CCAGGGCCAC TGCGAGGGGG GCTGGGCCAG TGCACCTTCC AGGGCTCCGT      1642
CCAGTAGTTT CCCCTGCCTT AATGTGACAT GAGGCCCATT CTTCTCTCTT      1692
TGAAGAGAGC AGTCAACATT CTTAGTAGTG GGTTTCTGTT CTATTGGATG      1742
ACTTTGAGAT TTGTCTTTGT TTCCTTTTGG AATTGTTCAA ATGTTCCTTT      1792
TAATGGGTGG TTGAATGAAC TTCAGCATTC AAATTTATGA ATGACAGTAG      1842
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TCACACATAG TGCTGTTTAT ATAGTTTAGG AGTAAGAGTC TTGTTTTTTA   1892
TTCAGATTGG GAAATCCATT CCATTTTGTG AATTGGGACA TAGTTACAGC   1942
AGTGGAATAA GTATTCATTT AGAAATGTGA ATGAGCAGTA AAACTGATGA   1992
GATAAAGAAA TTAAAAGATA TTTAATTCTT GCCTTATACT CAGTCTATTC   2042
GGTAAAATTT TTTTTTAAAA ATGTGCATAC CTGGATTTCC TTGGCTTCTT   2092
TGAGAATGTA AGACAAATTA AATCTGAATA AATCATTCTC CCTGTTCACT   2142
GGCTCATTTA TTCTCTATGC ACTGAGCATT TGCTCTGTGG AAGGCCCTGG   2192
GTTAATAGTG GAGATGCTAA GGTAAGCCAG ACTCACCCCT ACCCACAGGG   2242
TAGTAAAGTC TAGGAGCAGC AGTCATATAA TTAAGGTGGA GAGATGCCCT   2292
CTAAGATGTA GAG   2305

(2)   INFORMATION FOR SEQUENCE ID NO: 18:
      (i)   SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 225 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear
      (ii) MOLECULE TYPE: cDNA
      (ix) FEATURE:
            (A) NAME/KEY: MAGE-6 gene
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

TAT TTC TTT CCT GTG ATC TTC AGC AAA GCT TCC GAT TCC TTG   42
CAG CTG GTC TTT GGC ATC GAG CTG ATG GAA GTG GAC CCC ATC   84
GGC CAC GTG TAC ATC TTT GCC ACC TGC CTG GGC CTC TCC TAC   126
GAT GGC CTG CTG GGT GAC AAT CAG ATC ATG CCC AGG ACA GGC   168
TTC CTG ATA ATC ATC CTG GCC ATA ATC GCA AGA GAG GGC GAC   210
TGT GCC CCT GAG GAG   225

(2)   INFORMATION FOR SEQUENCE ID NO: 19:
      (i)   SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 1947 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear
      (ii) MOLECULE TYPE: genomic DNA
      (ix) FEATURE:
            (A) NAME/KEY: MAGE-7 gene
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

TGAATGGACA ACAAGGGCCC CACACTCCCC AGAACACAAG GGACTCCAGA   50
GAGCCCAGCC TCACCTTCCC TACTGTCAGT CCTGCAGCCT CAGCCTCTGC   100
TGGCCGGCTG TACCCTGAGG TGCCCTCTCA CTTCCTCCTT CAGGTTCTCA   150
GCGGACAGGC CGGCCAGGAG GTCAGAAGCC CCAGGAGGCC CCAGAGGAGC   200

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ACCGAAGGAG AAGATCTGTA AGTAGGCCTT TGTTAGGGCC TCCAGGGCGT          250
GGTTCACAAA TGAGGCCCCT CACAAGCTCC TTCTCTCCCC AGATCTGTGG          300
GTTCCTCCCC ATCGCCCAGC TGCTGCCCGC ACTCCAGCCT GCTGCCCTGA          350
CCAGAGTCAT CATGTCTTCT GAGCAGAGGA GTCAGCACTG CAAGCCTGAG          400
GATGCCTTGA GGCCCAAGGA CAGGAGGCTC TGGGCCTGGT GGGTGCGCAG          450
GCTCCCGCCA CCGAGGAGCA CGAGGCTGCC TCCTCCTTCA CTCTGATTGA          500
AGGCACCCTG GAGGAGGTGC CTGCTGCTGG GTCCCCCAGT CCTCCCCTGA          550
GTCTCAGGGT TCCTCCTTTT CCCTGACCAT CAGCAACAAC ACTCTATGGA          600
GCCAATCCAG TGAGGGCACC AGCAGCCGGG AAGAGGAGGG GCCAACCACC          650
TAGACACACC CCGCTCACCT GGCGTCCTTG TTCCA                          685
ATG GGA AGG TGG CTG AGT TGG TTC GCT TCC TGC TGC ACA AGT          727
ATC GAG TCA AGG AGC TGG TCA CAA AGG CAG AAA TGC TGG ACA          769
GTG TCA TCA AAA ATT ACA AGC ACT AGT TTC CTT GTG ATC TAT          811
GGC AAA GCC TCA GAG TGC ATG CAG GTG ATG TTT GGC ATT GAC          853
ATG AAG GAA GTG GAC CCC GCG GCC ACT CCT ACG TCC TTG TCA          895
CCT GCT TGG GCC TCT CCT ACA ATG GCC TGC TGG GTG ATG ATC          937
AGA GCA TGC CCG AGA CCG GCC TTC TGA                              964
TTATGGTCTT GACCATGATC TTAATGGAGG GCCACTGTGC CCCTGAGGAG         1014
GCAATCTGGG AAGCGTTGAG TGTAATGGTG TATGATGGGA TGGAGCAGTT         1064
TCTTTGGGCA GCTGAGGAAG CTGCTCACCC AAGATTGGGT GCAGGAAAAC         1114
TACCTGCAAT ACCGCCAGGT GCCCAGCAGT GATCCCCCGT GCTACCAGTT         1164
CCTGTGGGGT CCAAGGGCCC TCATTGAAAC CAGCTATGTG AAAGTCCTGG         1214
AGTATGCAGC CAGGGTCAGT ACTAAAGAGA GCATTTCCTA CCCATCCCTG         1264
CATGAAGAGG CTTTGGGAGA GGAGGAAGAG GGAGTCTGAG CAGAAGTTGC         1314
AGCCAGGGCC AGTGGGGCAG ATTGGGGGAG GGCCTGGGCA GTGCACGTTC         1364
CACACATCCA CCACCTTCCC TGTCCTGTTA CATGAGGCCC ATTCTTCACT         1414
CTGTGTTTGA AGAGAGCAGT CAATGTTCTC AGTAGCGGGG AGTGTGTTGG         1464
GTGTGAGGGA ATACAAGGTG GACCATCTCT CAGTTCCTGT TCTCTTGGGC         1514
GATTTGGAGG TTTATCTTTG TTTCCTTTTG CAGTCGTTCA AATGTTCCTT         1564
TTAATGGATG GTGTAATGAA CTTCAACATT CATTTCATGT ATGACAGTAG         1614
GCAGACTTAC TGTTTTTTAT ATAGTTAAAA GTAAGTGCAT TGTTTTTTAT         1664
TTATGTAAGA AAATCTATGT TATTTCTTGA ATTGGGACAA CATAACATAG         1714
CAGAGGATTA AGTACCTTTT ATAATGTGAA AGAACAAAGC GGTAAAATGG         1764
GTGAGATAAA GAAATAAAGA AATTAAATTG GCTGGGCACG GTGGCTCACG         1814
CCTGTAATCC CAGCACTTTA GGAGGCAGAG GCACGGGGAT CACGAGGTCA         1864
GGAGATCGAG ACCATTCTGG CTAACACAGT GAAACACCAT CTCTATTAAA         1914
AATACAAAAC TTAGCCGGGC GTGGTGGCGG GTG                           1947
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(2)   INFORMATION FOR SEQUENCE ID NO: 20:
       (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 1810 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear
       (ii) MOLECULE TYPE: genomic DNA
       (ix) FEATURE:
            (A) NAME/KEY: MAGE-8 gene
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

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GTTCCTCCCC ATCGCCCAGC TGCTGCCCGC ACTCCAGCCT GCTGCCCTGA          350
CCAGAGTCAT CATGTCTTCT GAGCAGAGGA GTCAGCACTG CAAGCCTGAG          400
GATGCCTTGA GGCCCAAGGA CAGGAGGCTC TGGGCCTGGT GGGTGCGCAG          450
GCTCCCGCCA CCGAGGAGCA CGAGGCTGCC TCCTCCTTCA CTCTGATTGA          500
AGGCACCCTG GAGGAGGTGC CTGCTGCTGG GTCCCCCAGT CCTCCCCTGA          550
GTCTCAGGGT TCCTCCTTTT CCCTGACCAT CAGCAACAAC ACTCTATGGA          600
GCCAATCCAG TGAGGGCACC AGCAGCCGGG AAGAGGAGGG GCCAACCACC          650
TAGACACACC CCGCTCACCT GGCGTCCTTG TTCCA                         685
ATG GGA AGG TGG CTG AGT TGG TTC GCT TCC TGC TGC ACA AGT         727
ATC GAG TCA AGG AGC TGG TCA CAA AGG CAG AAA TGC TGG ACA         769
GTG TCA TCA AAA ATT ACA AGC ACT AGT TTC CTT GTG ATC TAT         811
GGC AAA GCC TCA GAG TGC ATG CAG GTG ATG TTT GGC ATT GAC         853
ATG AAG GAA GTG GAC CCC GCG GCC ACT CCT ACG TCC TTG TCA         895
CCT GCT TGG GCC TCT CCT ACA ATG GCC TGC TGG GTG ATG ATC         937
AGA GCA TGC CCG AGA CCG GCC TTC TGA                             964
TTATGGTCTT GACCATGATC TTAATGGAGG GCCACTGTGC CCCTGAGGAG         1014
GCAATCTGGG AAGCGTTGAG TGTAATGGTG TATGATGGGA TGGAGCAGTT         1064
TCTTTGGGCA GCTGAGGAAG CTGCTCACCC AAGATTGGGT GCAGGAAAAC         1114
TACCTGCAAT ACCGCCAGGT GCCCAGCAGT GATCCCCCGT GCTACCAGTT         1164
CCTGTGGGGT CCAAGGGCCC TCATTGAAAC CAGCTATGTG AAAGTCCTGG         1214
AGTATGCAGC CAGGGTCAGT ACTAAAGAGA GCATTTCCTA CCCATCCCTG         1264
CATGAAGAGG CTTTGGGAGA GGAGGAAGAG GGAGTCTGAG CAGAAGTTGC         1314
AGCCAGGGCC AGTGGGGCAG ATTGGGGGAG GGCCTGGGCA GTGCACGTTC         1364
CACACATCCA CCACCTTCCC TGTCCTGTTA CATGAGGCCC ATTCTTCACT         1414
CTGTGTTTGA AGAGAGCAGT CAATGTTCTC AGTAGCGGGG AGTGTGTTGG         1464
GTGTGAGGGA ATACAAGGTG GACCATCTCT CAGTTCCTGT TCTCTTGGGC         1514
GATTTGGAGG TTTATCTTTG TTTCCTTTTG CAGTCGTTCA AATGTTCCTT         1564
TTAATGGATG GTGTAATGAA CTTCAACATT CATTTCATGT ATGACAGTAG         1614
GCAGACTTAC TGTTTTTTAT ATAGTTAAAA GTAAGTGCAT TGTTTTTTAT         1664
TTATGTAAGA AAATCTATGT TATTTCTTGA ATTGGGACAA CATAACATAG         1714
CAGAGGATTA AGTACCTTTT ATAATGTGAA AGAACAAAGC GGTAAAATGG         1764
GTGAGATAAA GAAATAAAGA AATTAAATTG GCTGGGCACG GTGGCTCACG         1814
CCTGTAATCC CAGCACTTTA GGAGGCAGAG GCACGGGGAT CACGAGGTCA         1864
GGAGATCGAG ACCATTCTGG CTAACACAGT GAAACACCAT CTCTATTAAA         1914
AATACAAAAC TTAGCCGGGC GTGGTGGCGG GTG                           1947
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(2)   INFORMATION FOR SEQUENCE ID NO: 20:
       (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 1810 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear
       (ii) MOLECULE TYPE: genomic DNA
       (ix) FEATURE:
           (A) NAME/KEY: MAGE-8 gene
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

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ACCCCACAGT TCCTGGCCCT ACCAGCCCTT TTGTCAGTCC TGGAGCCTTG         200
GCCTTTGCCA GGAGGCTGCA CCCTGAGATG CCCTCTCAAT TTCTCCTTCA         250
GGTTCGCAGA GAACAGGCCA GCCAGGAGGT CAGGAGGCCC CAGAGAAGCA         300
CTGAAGAAGA CCTGTAAGTA GACCTTTGTT AGGGCATCCA GGGTGTAGTA         350
CCCAGCTGAG GCCTCTCACA CGCTTCCTCT CTCCCCAGGC CTGTGGGTCT         400
CAATTGCCCA GCTCCGGCCC ACACTCTCCT GCTGCCCTGA CCTGAGTCAT         450
C                                                             451
ATG CTT CTT GGG CAG AAG AGT CAG CGC TAC AAG GCT GAG GAA        493
GGC CTT CAG GCC CAA GGA GAG GCA CCA GGG CTT ATG GAT GTG        535
CAG ATT CCC ACA GCT GAG GAG CAG AAG GCT GCA TCC TCC TCC        577
TCT ACT CTG ATC ATG GGA ACC CTT GAG GAG GTG ACT GAT TCT        619
GGG TCA CCA AGT CCT CCC CAG AGT CCT GAG GGT GCC TCC TCT        661
TCC CTG ACT GTC ACC GAC AGC ACT CTG TGG AGC CAA TCC GAT        703
GAG GGT.TCC AGC AGC AAT GAA GAG GAG GGG CCA AGC ACC TCC        745
CCG GAC CCA GCT CAC CTG GAG TCC CTG TTC CGG GAA GCA CTT        787
GAT GAG AAA GTG GCT GAG TTA GTT CGT TTC CTG CTC CGC AAA        829
TAT CAA ATT AAG GAG CCG GTC ACA AAG GCA GAA ATG CTT GAG        871
AGT GTC ATC AAA AAT TAC AAG AAC CAC TTT CCT GAT ATC TTC        913
AGC AAA GCC TCT GAG TGC ATG CAG GTG ATC TTT GGC ATT GAT        955
GTG AAG GAA GTG GAC CCT GCC GGC CAC TCC TAC ATC CTT GTC        997
ACC TGC CTG GGC CTC TCC TAT GAT GGC CTG CTG GGT GAT GAT       1039
CAG AGT ACG CCC AAG ACC GGC CTC CTG ATA ATC GTC CTG GGC       1081
ATG ATC TTA ATG GAG GGC AGC CGC GCC CCG GAG GAG GCA ATC       1123
TGG GAA GCA TTG AGT GTG ATG GGG GCT GTA TGA                   1156
TGGGAGGGAG CACAGTGTCT ATTGGAAGCT CAGGAAGCTG CTCACCCAAG        1206
AGTGGGTGCA GGAGAACTAC CTGGAGTACC GCCAGGCGCC CGGCAGTGAT        1256
CCTGTGCGCT ACGAGTTCCT GTGGGGTCCA AGGGCCCTTG CTGAAACCAG        1306
CTATGTGAAA GTCCTGGAGC ATGTGGTCAG GGTCAATGCA AGAGTTCGCA        1356
TTTCCTACCC ATCCCTGCAT GAAGAGGCTT TGGGAGAGGA GAAAGGAGTT        1406
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ATTC                                                         1810
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(2)   INFORMATION FOR SEQUENCE ID NO: 21:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1412 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: genomic DNA
    (ix) FEATURE:

(A) NAME/KEY: MAGE-9 gene
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:


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TCACTCATAG AGCCTTGATC TCTGCAGGCT AGCTGCACGC TGAGTAGCCC         200
TCTCACTTCC TCCCTCAGGT TCTCGGGACA GGCTAACCAG GAGGACAGGA         250
GCCCCAAGAG GCCCCAGAGC AGCACTGACG AAGACCTGTA AGTCAGCCTT         300
TGTTAGAACC TCCAAGGTTC GGTTCTCAGC TGAAGTCTCT CACACACTCC         350
CTCTCTCCCC AGGCCTGTGG GTCTCCATCG CCCAGCTCCT GCCCACGCTC         400
CTGACTGCTG CCCTGACCAG AGTCATC                                  427
ATG TCT CTC GAG CAG AGG AGT CCG CAC TGC AAG CCT GAT GAA        469
GAC CTT GAA GCC CAA GGA GAG GAC TTG GGC CTG ATG GGT GCA        511
CAG GAA CCC ACA GGC GAG GAG GAG GAG ACT ACC TCC TCC TCT        553
GAC AGC AAG GAG GAG GAG GTG TCT GCT GCT GGG TCA TCA AGT        595
CCT CCC CAG AGT CCT CAG GGA GGC GCT TCC TCC TCC ATT TCC        637
GTC TAC TAC ACT TTA TGG AGC CAA TTC GAT GAG GGC TCC AGC        679
AGT CAA GAA GAG GAA GAG CCA AGC TCC TCG GTC GAC CCA GCT        721
CAG CTG GAG TTC ATG TTC CAA GAA GCA CTG AAA TTG AAG GTG        763
GCT GAG TTG GTT CAT TTC CTG CTC CAC AAA TAT CGA GTC AAG        805
GAG CCG GTC ACA AAG GCA GAA ATG CTG GAG AGC GTC ATC AAA        847
AAT TAC AAG CGC TAC TTT CCT GTG ATC TTC GGC AAA GCC TCC        889
GAG TTC ATG CAG GTG ATC TTT GGC ACT GAT GTG AAG GAG GTG        931
GAC CCC GCC GGC CAC TCC TAC ATC CTT GTC ACT GCT CTT GGC        973
CTC TCG TGC GAT AGC ATG CTG GGT GAT GGT CAT AGC ATG CCC       1015
AAG GCC GCC CTC CTG ATC ATT GTC CTG GGT GTG ATC CTA ACC       1057
AAA GAC AAC TGC GCC CCT GAA GAG GTT ATC TGG GAA GCG TTG       1099
AGT GTG ATG GGG GTG TAT GTT GGG AAG GAG CAC ATG TTC TAC       1141
GGG GAG CCC AGG AAG CTG CTC ACC CAA GAT TGG GTG CAG GAA       1183
AAC TAC CTG GAG TAC CGG CAG GTG CCC GGC AGT GAT CCT GCG       1225
CAC TAC GAG TTC CTG TGG GGT TCC AAG GCC CAC GCT GAA ACC       1267
AGC TAT GAG AAG GTC ATA AAT TAT TTG GTC ATG CTC AAT GCA       1309
AGA GAG CCC ATC TGC TAC CCA TCC CTT TAT GAA GAG GTT TTG       1351
GGA GAG GAG CAA GAG GGA GTC TGA                               1375
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(2) INFORMATION FOR SEQUENCE ID NO: 22:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 920 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: genomic DNA
     (ix) FEATURE:
          (A) NAME/KEY: MAGE-10 gene
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

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CTCTCACTTC CTTCTTCAGG TTCTCAGGGG ACAGGGAGAG CAAGAGGTCA       150
AGAGCTGTGG GACACCACAG AGCAGCACTG AAGGAGAAGA CCTGTAAGTT       200
GGCCTTTGTT AGAACCTCCA GGGTGTGGTT CTCAGCTGTG GCCACTTACA       250
CCCTCCCTCT CTCCCCAGGC CTGTGGGTCC CCATCGCCCA AGTCCTGCCC       300
ACACTCCCAC CTGCTACCCT GATCAGAGTC ATC                         333
ATG CCT CGA GCT CCA AAG CGT CAG CGC TGC ATG CCT GAA GAA       375
GAT CTT CAA TCC CAA AGT GAG ACA CAG GGC CTC GAG GGT GCA       417
CAG GCT CCC CTG GCT GTG GAG GAG GAT GCT TCA TCA TCC ACT       459
TCC ACC AGC TCC TCT TTT CCA TCC TCT TTT CCC TCC TCC TCC       501
TCT TCC TCC TCC TCC TCC TGC TAT CCT CTA ATA CCA AGC ACC       543
CCA GAG GAG GTT TCT GCT GAT GAT GAG ACA CCA AAT CCT CCC       585
CAG AGT GCT CAG ATA GCC TGC TCC TCC CCC TCG GTC GTT GCT       627
TCC CTT CCA TTA GAT CAA TCT GAT GAG GGC TCC AGC AGC CAA       669
AAG GAG GAG AGT CCA AGC ACC CTA CAG GTC CTG CCA GAC AGT       711
GAG TCT TTA CCC AGA AGT GAG ATA GAT GAA AAG GTG ACT GAT       753
TTG GTG CAG TTT CTG CTC TTC AAG TAT CAA ATG AAG GAG CCG       795
ATC ACA AAG GCA GAA ATA CTG GAG AGT GTC ATA AAA AAT TAT       837
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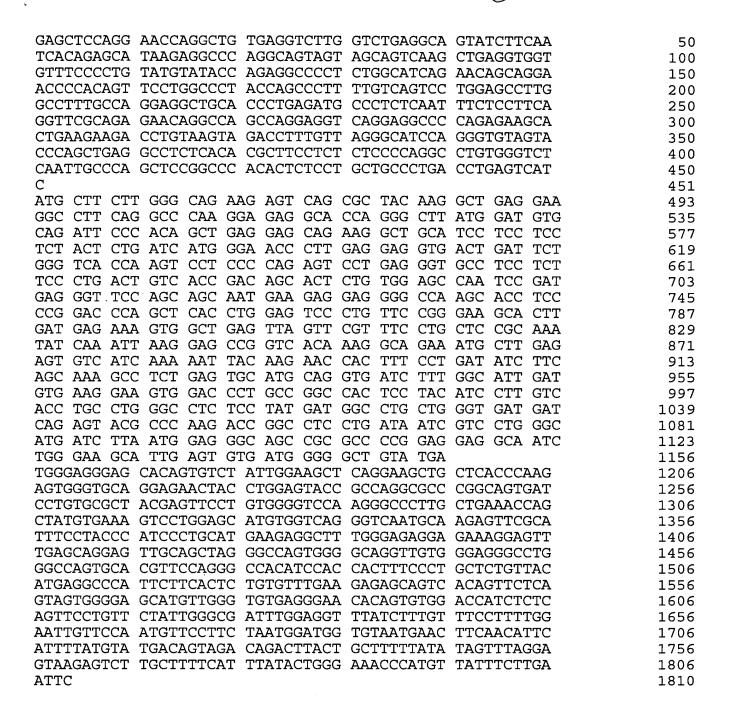

(2)   INFORMATION FOR SEQUENCE ID NO: 23:
       (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 1107 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear
       (ii) MOLECULE TYPE: genomic DNA
       (ix) FEATURE:
           (A) NAME/KEY: MAGE-11 gene
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:


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GGCCCCATCA CCCAGATATT TCCCACAGTT CGGCCTGCTG ACCTAACCAG       200
AGTCATCATG CCTCTTGAGC AAAGAAGTCA GCACTGCAAG CCTGAGGAAG       250
CCTTCAGGCC CAAGAAGAAG ACCTGGGCCT GGTGGGTGCA CAGGCTCTCC       300
AAGCTGAGGA GCAGGAGGCT GCCTTCTTCT CCTCTACTCT GAATGTGGGC       350
ACTCTAGAGG AGTTGCCTGC TGCTGAGTCA CCAAGTCCTC CCCAGAGTCC       400
TCAGGAAGAG TCCTTCTCTC CCACTGCCAT GGATGCCATC TTTGGGAGCC       450
TATCTGATGA GGGCTCTGGC AGCCAAGAAA AGGAGGGGCC AAGTACCTCG       500
CCTGACCTGA TAGACCCTGA GTCCTTTTCC CAAGATATAC TACATGACAA       550
GATAATTGAT TTGGTTCATT TATTCTCCGC AAGTATCGAG TCAAGGGGCT       600
GATCACAAAG GCAGAA                                            616
ATG CTG GGG AGT GTC ATC AAA AAT TAT GAG GAC TAC TTT CCT       658
GAG ATA TTT AGG GAA GCC TCT GTA TGC ATG CAA CTG CTC TTT       700
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GTC CTT GTC ACC TCC CTC AAC CTC TCT TAT GAT GGC ATA CAG        784
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GTC CTG GGT GTA ATC TTC ATG GAG GGG AAC TGC ATC CCT GAA        868
GAG GTT ATG TGG GAA GTC CTG AGC ATT ATG GGG GTG TAT GCT        910
GGA AGG GAG CAC TTC CTC TTT GGG GAG CCC AAG AGG CTC CTT        952
ACC CAA AAT TGG GTG CAG GAA AAG TAC CTG GTG TAC CGG CAG        994
GTG CCC GGC ACT GAT CCT GCA TGC TAT GAG TTC CTG TGG GGT       1036
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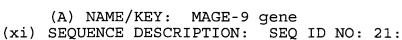
(2) INFORMATION FOR SEQUENCE ID NO: 24:
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        (A) LENGTH: 2150 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: genomic DNA
    (ix) FEATURE:
        (A) NAME/KEY: smage-I
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

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ACAGGTTTCT GCCCCTGCAT GGAGCTTAAA TAGATCTTTC TCCACAGGCC       150
TATACCCCTG CATTGTAAGT TTAAGTGGCT TTATGTGGAT ACAGGTCTCT       200
GCCCTTGTAT GCAGGCCTAA GTTTTTCTGT CTGCTTAACC CCTCCAAGTG       250
AAGCTAGTGA AAGATCTAAC CCACTTTTGG AAGTCTGAAA CTAGACTTTT       300
ATGCAGTGGC CTAACAAGTT TTAATTTCTT CCACAGGGTT TGCAGAAAAG       350
AGCTTGATCC ACGAGTTCAG AAGTCCTGGT ATGTTCCTAG AAAG            394
ATG TTC TCC TGG AAA GCT TCA AAA GCC AGG TCT CCA TTA AGT       436
CCA AGG TAT TCT CTA CCT GGT AGT ACA GAG GTA CTT ACA GGT       478
TGT CAT TCT TAT CCT TCC AGA TTC CTG TCT GCC AGC TCT TTT       520
ACT TCA GCC CTG AGC ACA GTC AAC ATG CCT AGG GGT CAA AAG       565
AGT AAG ACC CGC TCC CGT GCA AAA CGA CAG CAG TCA CGC AGG       604
GAG GTT CCA GTA GTT CAG CCC ACT GCA GAG GAA GCA GGG TCT       646
TCT CCT GTT GAC CAG AGT GCT GGG TCC AGC TTC CCT GGT GGT       688
TCT GCT CCT CAG GGT GTG AAA ACC CCT GGA TCT TTT GGT GCA       730
GGT GTA TCC TGC ACA GGC TCT GGT ATA GGT GGT AGA AAT GCT       772
GCT GTC CTG CCT GAT ACA AAA AGT TCA GAT GGC ACC CAG GCA       814
GGG ACT TCC ATT CAG CAC ACA CTG AAA GAT CCT ATC ATG AGG       856
AAG GCT AGT GTG CTG ATA GAA TTC CTG CTA GAT AAA TTT AAG       898
ATG AAA GAA GCA GTT ACA AGG AGT· GAA ATG CTG GCA GTA GTT       940
AAC AAG AAG TAT AAG GAG CAA TTC CCT GAG ATC CTC AGG AGA       982
ACT TCT GCA CGC CTA GAA TTA GTC TTT GGT CTT GAG TTG AAG      1024
GAA ATT GAT CCC AGC ACT CAT TCC TAT TTG CTG GTA GGC AAA      1066
CTG GGT CTT TCC ACT GAG GGA AGT TTG AGT AGT AAC TGG GGG      1108
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CCA AGC TAT GAG TTC CTG TGG GGA CCC AGA GCC CAT GCT GAA      1360
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CTT AGA GAT CAG GCA GGA GGG GTG CCA AGA AGG AGA GTT CAA      1486
GGC AAG GGT GTT CAT TCC AAG GCC CCA TCC CAA AAG TCC TCT      1528
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GATTGTCATG GCAATGTGAT ATCATACAGT GGTGAAACAA CAGTGAAGTG          1887
GGAAAGTTTA TATTGTTAAT TTTGAAAATT TTATGAGTGT GATTGCTGTA          1937
TACTTTTTTC TTTTTTGTAT AATGCTAAGT GAAATAAAGT TGGATTTGAT          1987
GACTTTACTC AAATTCATTA GAAAGTAAAT CGTAAAACTC TATTACTTTA          2037
TTATTTTCTT CAATTATGAA TTAAGCATTG GTTATCTGGA AGTTTCTCCA          2087
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        (2)    INFORMATION FOR SEQUENCE ID NO: 25:
               (i) SEQUENCE CHARACTERISTICS:
                   (A) LENGTH:  2099 base pairs
                   (B) TYPE:    nucleic acid
                   (C) STRANDEDNESS: single
                   (D) TOPOLOGY:  linear
               (ii) MOLECULE TYPE:  genomic DNA
               (ix) FEATURE:
                   (A) NAME/KEY:  smage-II
               (xi) SEQUENCE DESCRIPTION:  SEQ ID NO: 25:


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CTCCACAGGC CTATACCCCT GCATTGTAAG TTTAAGTGGC TTTATGTGGA           200
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CCCTCCAAGT GAAGCTAGTG AAAGATCTAA CCCACTTTTG GAAGTCTGAA           300
ACTAGACTTT TATGCAGTGG CCTAACAAGT TTTAATTTCT TCCACAGGGT           350
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GAAAGATGTT CTCCTGGAAA GCTTCAAAAG CCAGGTCTCC ATTAAGTCCA           450
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CAGCAGTCAC GCAGGGAGGT TCCAGTAGTT CAGCCCACTG CAGAGGAAGC           650
AGGGTCTTCT CCTGTTGACC AGAGTGCTGG GTCCAGCTTC CCTGGTGGTT           700
CTGCTCCTCA GGGTGTGAAA ACCCCTGGAT CTTTTGGTGC AGGTGTATCC           750
TGCACAGGCT CTGGTATAGG TGGTAGAAAT GCTGCTGTCC TGCCTGATAC           800
AAAAAGTTCA GATGGCACCC AGGCAGGGAC TTCCATTCAG CACACACTGA           850
AAGATCCTAT CATGAGGAAG GCTAGTGTGC TGATAGAATT CCTGCTAGAT           900
AAGTTTAAGA TGAAAGAAGC AGTTACAAGG AGTGAAATGC TGGCAGTAGT           950
TAACAAGAAG TATAAGGAGC AATTCCCTGA GATCCTCAGG AGAACTTCTG          1000
CACGCCTAGA ATTAGTCTTT GGTCTTGAGT TGAAGGAAAT TGATCCCAGC          1050
ACTCATTCCT ATTTGCTGGT AGGCAAACTG GGTCTTTCCA CTGAGGGAAG          1100
TTTGAGTAGT AACTGGGGGT TGCCTAGGAC AGGTCTCCTA ATGTCTGTCC          1150
TAGGTGTGAT CTTCATGAAG GGTAACCGTG CCACTGAGCA AGAGGTCTGG          1200
CAATTTCTGC ATGGAGTGGG GGTATATGCT GGGAAGAAGC ACTTGATCTT          1250
TGGCGAGCCT GAGGAGTTTA TAAGAGATGT AGTGCGGGAA AATTACCTGG          1300
AGTACCGCCA GGTACCTGGC AGTGATCCCC CAAGCTATGA GTTCCTGTGG          1350
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GGACCCAGAG CCCATGCTGA AACAACCAAG ATGAAAGTCC TGGAAGTTTT        1400
AGCTAAAGTC AATGGCACAG TCCCTAGTGC CTTCCCTAAT CTCTACCAGT        1450
TGGCTCTTAG AGATCAGGCA GGAGGGGTGC CAAGAAGGAG AGTTCAAGGC        1500
AAGGGTGTTC ATTCCAAGGC CCCATCCCAA AAGTCCTCTA ACATGTAGTT        1550
GAGTCTGTTC TGTTGTGTTT GAAAAACAGT CAGGCTCCTA ATCAGTAGAG        1600
AGTTCATAGC CTACCAGAAC CAACATGCAT CCATTCTTGG CCTGTTATAC        1650
ATTAGTAGAA TGGAGGCTAT TTTTGTTACT TTTCAAATGT TTGTTTAACT        1700
AAACAGTGCT TTTTGCCATG CTTCTTGTTA ACTGCATAAA GAGGTAACTG        1750
TCACTTGTCA GATTAGGACT TGTTTTGTTA TTTGCAACAA ACTGGAAAAC        1800
ATTATTTTGT TTTTACTAAA ACATTGTGTA ACATTGCATT GGAGAAGGGA        1850
TTGTCATGGC AATGTGATAT CATACAGTGG TGAAACAACA GTGAAGTGGG        1900
AAAGTTTATA TTGTTAGTTT TGAAAATTTT ATGAGTGTGA TTGCTGTATA        1950
CTTTTTTCTT TTTTGTATAA TGCTAAGTGA AATAAAGTTG GATTTGATGA        2000
CTTTACTCAA ATTCATTAGA AAGTAAATCA TAAAACTCTA TTACTTTATT        2050
ATTTTCTTCA ATTATTAATT AAGCATTGGT TATCTGGAAG TTTCTCCAG         2099
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(2)   INFORMATION FOR SEQUENCE ID NO: 26:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 9 amino acids
        (B) TYPE: amino acids
        (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: protein
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Glu Ala Asp Pro Thr Gly His Ser Tyr
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